

High-order remapping using MOOD paradigm

(Multi-dimensional Optimal Order Detection)

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MOOD : Multi-dimensional Optimal Order Detection

Context

MOOD method stated and developed during S.Diot's PhD (2009-2012) with S.Clain (U. do Minho, Portugal) as co-mentor. Full implementation and testing has been done by S.Diot.

Purposes

- New class of FV numerical methods for hyperbolic systems
- High order polynomial reconstruction to get high accuracy
- At least recover state of the art results (accuracy, efficiency)

Design principles

- Genuinely multidimensional Eulerian finite volume on unstructured meshes
- Arbitrary high-order polynomial reconstruction
- Detect the 'optimal polynomial degree' (stable, robust, accurate)

Bibliography

- [1] S. Diot, R. Loubère, S. Clain, The MOOD method in the three-dimensional case : Very-High-Order Finite Volume Method for Hyperbolic Systems, Int. J. Numer. Meth. FLUIDS (2013).
- [2] S.D, S.C, R.L, Improved detection criteria for the Multi-dimensional Optimal Order Detection (MOOD) on unstructured meshes, Comput. Fluids 64 (2012) 43-63.
- [3] S.C, S.D, R.L, A high-order finite volume method for systems of conservation laws Multi-dimensional Optimal Order Detection (MOOD), J. Comput. Phys. 230 (2011)

MOOD : Multi-dimensional Optimal Order Detection

Philosophy

High order FV schemes need some sort of limitation

- MUSCL (Kolgan, Van Leer...) : piecewise linear reconstruction + limiter to enforce bounds
- (W)ENO (Shu, Osher...) : arbitrary polynomial reconstruction + non-linear combination of polynomials to get ENO behavior

Slope limiter – An *a priori* process based on

- 1 'Worst case scenario' – Over/undershoot of reconstructions are premisses of oscillations !
- 2 'Precautional principle' – I preventively must act to avoid creation of new extrema
- 3 'Prediction capability' – Given solution at t^n , I KNOW when/how my scheme does misbehave

However

- 1 'Worst case scenario' – Increase of mean value does not imply occurrence of an oscillation
- 2 'Precautional principle' – Is it always/often legitimate to act ?
- 3 'Prediction capability' – Can I truly predict the scheme's reaction to NL behaviors ?

→ Why not ? Try, (possibly locally) Fail then *a posteriori* Detect and Repair → MOOD

MOOD : Multi-dimensional Optimal Order Detection

MOOD *a posteriori* detection criteria — #1 Convection equation

Transport of a scalar quantity

$$\partial_t u + \nabla \cdot (V u) = 0, \quad \text{with} \quad V = V(\mathbf{x}) \in \mathbb{R}^m, \quad u \in \mathbb{R}$$

If $\nabla \cdot V = 0$ then solution fulfills a maximum principle. u^* numerical solution given by highest polynomial degrees \Rightarrow unlimited !

Detection Process : Discrete Maximum Principle (DMP) as 1st filter

Check if u_i^* fulfills the DMP $\min_{j \in \bar{\nu}(i)}(u_j^n, u_j^n) \leq u_i^* \leq \max_{j \in \bar{\nu}(i)}(u_j^n, u_j^n)$

If detection is strict on {DMP} \Rightarrow 2nd-order error at smooth extrema \Rightarrow DMP violation must be allowed at smooth extrema to reach higher orders !

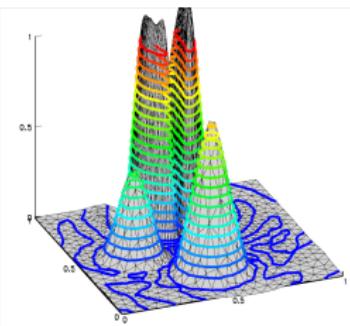
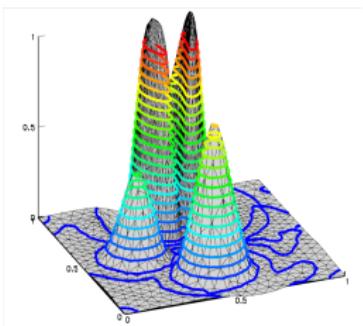
Detection Process : u2 as 2nd filter \rightarrow Distinguish discontinuities and smooth extrema

A solution violating the DMP is nonetheless acceptable if

$$\mathcal{W}_i^{\min} \mathcal{W}_i^{\max} > 0 \quad (\text{Non oscillatory}) \quad \text{and} \quad \left| \mathcal{W}_i^{\min} / \mathcal{W}_i^{\max} \right| > 1 - \varepsilon = 1/2 \quad (\text{Smoothness})$$

where $\mathcal{W}_i^{\min} = \min_{j \in \bar{\nu}(i)}(\mathcal{W}_j, \mathcal{W}_i)$, $\mathcal{W}_i^{\max} = \max_{j \in \bar{\nu}(i)}(\mathcal{W}_j, \mathcal{W}_i)$ with $\mathcal{X}_j = \partial_{xx} \tilde{U}_j$, $\mathcal{Y}_j = \partial_{yy} \tilde{U}_j$, $\mathcal{Z}_j = \partial_{zz} \tilde{U}_j$ with $\tilde{U}_j \in \mathbb{P}^2$ (reconstructed sol.)

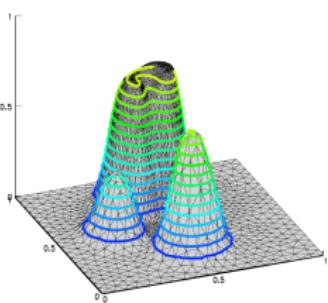
Results : Solid Body Rotation in 2D (5190 triangles)



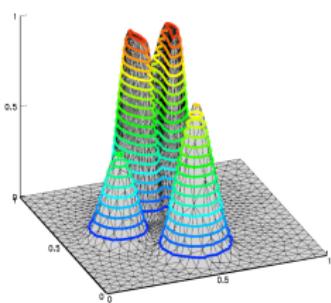
Exact

UNLIM-P3

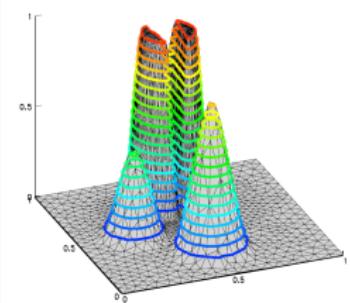
UNLIM-P5



MUSCL

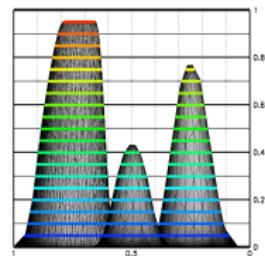


MOOD-P3

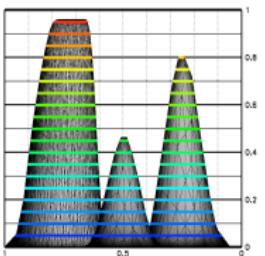


MOOD-P5

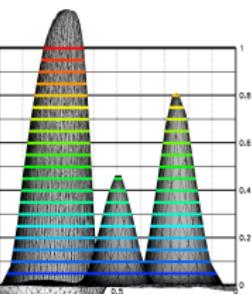
Results : Solid Body Rotation in 2D (5190 triangles)



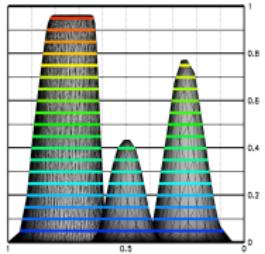
MOOD-P3 DMP



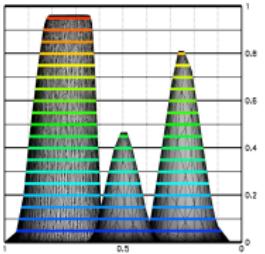
MOOD-P3 U2



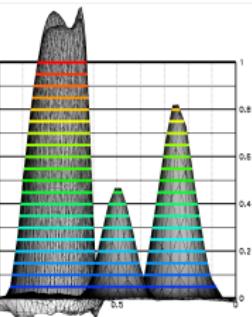
UNLIM-P3



MOOD-P5 DMP



MOOD-P5 U2



UNLIM-P5

Remapping using MOOD paradigm

Towards an effective *a posteriori* very high-order remapping

Remapping of given profiles demands

- ① Exact or approximate intersection btw starting and target meshes ← geometrical error
- ② Reconstruction of variables of interest ← representation error
- ③ Exact/Numerical integration of reconstructions over overlays ← integration error

“Classical 2D remapping techniques” involve

- ① Exact intersection (no geometrical error), or swept or hybrid methods (2nd order error)
- ② Piecewise-Linear (PL) reconstruction using limiters (2nd order error on smooth profile)
- ③ Exact integration of reconstructions (no integration error)

(Very) high-order remapping technique demands

- Exact intersection and exact integration
- High-order reconstructions, as instance polynomials of degree 1 to 5
- Limiter for polynomials ? Huh ! . . . à la MOOD by reducing the polynomial degrees.

Note : a similar *a posteriori* treatment (reduction of gradient in PL reconstr. to fulfill DMP) can be found in P. Hoch. An ALE strategy to solve compressible fluid flows. HAL, 2009. hal.archives-ouvertes.fr/hal-00366858

High-order remapping

a posteriori MOOD

Exact mesh intersection

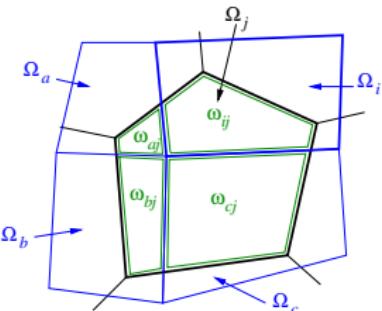
Starting mesh : $\mathcal{M} = \bigcup_i \Omega_i$, and target mesh : $\widetilde{\mathcal{M}} = \bigcup_j \widetilde{\Omega}_j$.

Intersection :

$$\widetilde{\Omega}_j = \bigcup_i (\Omega_i \cap \widetilde{\Omega}_j) = \bigcup_i \omega_{ij},$$

ω_{ij} : intersection polygon (may be empty)

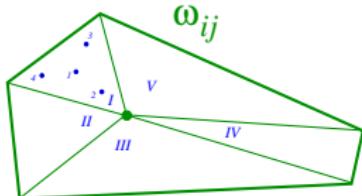
Note : in practice intersection-based remap in flux form on same topologies



Numerical integration

Integration of polynomial $A(\mathbf{X}) = \sum_{k=0}^d a_k \mathbf{X}^k$ over ω_{ij} using Gauss quadrature of appropriate accuracy

$$\int_{\omega_{ij}} A(\mathbf{X}) d\mathbf{X} = \bigcup_{O=1}^V \int_{T_O} A(\mathbf{X}) d\mathbf{X} = \sum_{O=1}^V \sum_{g=1}^G w_g^O A(\mathbf{X}_g^O)$$



High-order remapping

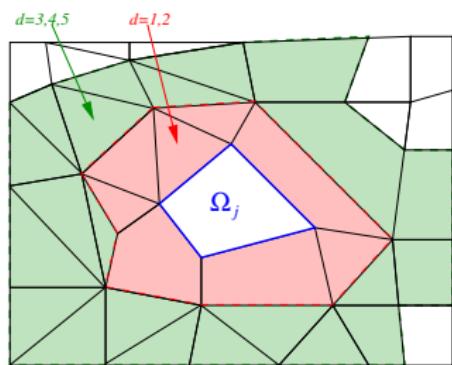
a posteriori MOOD

Polynomial reconstruction : Piecewise constant data per cell A_i

Polynomial of degree d centered on cell Ω_j

$$A(\mathbf{X}) = A_j + \sum_{1 \leq |k| \leq d} a_k \left((\mathbf{X} - \mathbf{X}_j)^k - \frac{1}{|\Omega_j|} \int_{\Omega_j} (\mathbf{X} - \mathbf{X}_j)^k d\mathbf{X} \right)$$

- In 2D need $\frac{(d+1)(d+2)}{2}$ neighbors (2, 5, 9, 14, 29 for $d = 1, 2, 3, 4, 5$)
- Neighborhoods are fixed. **Centered neighborhood !**
- a_k defined in the least square sense with respect to neighbor mean values
- Overdetermined system (QR decomp.), matrix precomputation



Boundary conditions and symmetry preservation

BCs : This is difficult even with ghost cells.

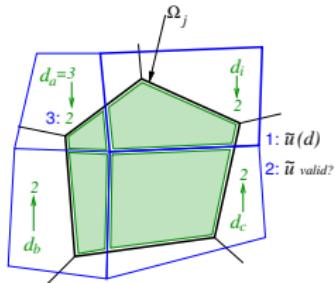
'Exact' symmetry preservation also difficult (with non symmetric mesh due to ill-conditionned system) → expect high resolution to help

High-order remapping

a posteriori MOOD

High-order MOOD paradigm

- 0 Set polynomial degrees $d_c = d^{max}$ in all old cells for all variables
- 1 Reconstruct polynomials (degree d_c). Remap without limitation
- 2 Validity of cell remapped solution given detection criteria \mathcal{D} ?
- 3 Decrement for invalid cells, $d_c = d_c - 1$
- 4 Back to 1 or exit (validity or $d_c = 0 \quad \forall c$)



Advantages

- Difficulty of defining *a priori* limiters for polynomials \mathbb{P}_k is discarded
- User can choose the sequence of decrementing (i.e 5, 3, 2, 0, or, 5, 2, 1lim) and the parachute final scheme (i.e \mathbb{P}_0 or \mathbb{P}_1 +limiter)
- Worst case : $d_c = 0$ and the parachute scheme is used for every cell and every variable

Difficulties

- Detection criteria set \mathcal{D} is the key and \mathcal{D} -friendly parachute scheme needed
- Iterative scheme : only bad cells are remapped several times.

High-order remapping

a posteriori MOOD. Advection equation.

High-order MOOD remapping of passive scalar :

Detection criteria $\mathcal{D} = f(\text{nature}(u))$

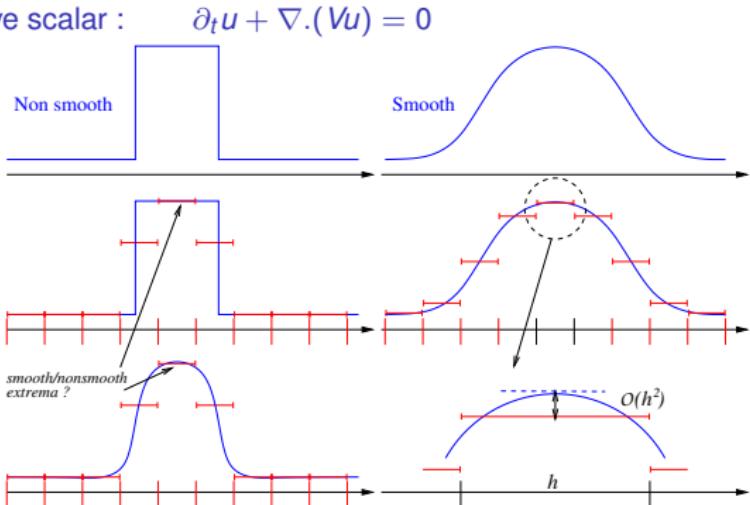
- Physical-exact bounds (MP)

$$0 \leq u_i \leq 1$$

- Numerical bounds (DMP) :

$$\min_{j \in \nu_i}(u_j) \leq u_i \leq \max_{j \in \nu_i}(u_j)$$

- Numerical smoothness and non-oscillation detection (using \mathbb{P}_2 reconstruction) : $u2$



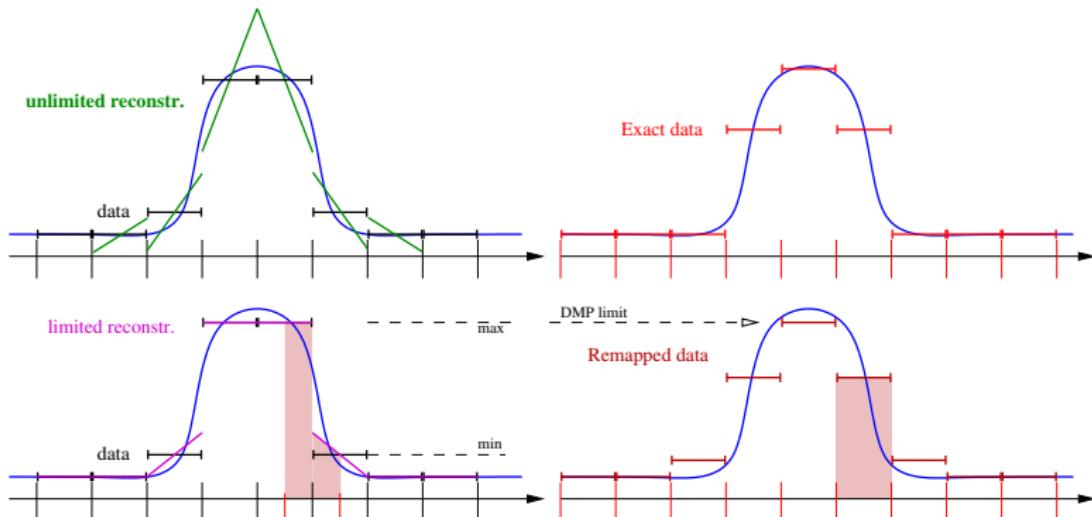
Numerical tests

1D cyclic remapping of profiles using \mathbb{P}_k , $k = 0, 1, 2, 3, 4, 5$ and MOOD decrementing. We test several detection criteria \mathcal{D} ($\mathcal{D} = \emptyset$ means unlimited).

High-order remapping

a posteriori MOOD.

Brief aside : Why DMP must be exceeded ? Example : shift mesh by $h/2$



Any *a priori* limiters fulfilling DMP can not capture smooth extrema with high accuracy.
 Nonetheless to avoid Gibbs phenomenon we must have some sort of limiting \Rightarrow *a priori*.

Note : (W)ENO limitation does not respect DMP, hence HO of accuracy !

I Cyclic remap — 128 cells/640 remaps — \mathbb{P}_0 , MUSCL, $\mathbb{P}_3/\mathbb{P}_5$ MOOD with U2

\mathbb{P}_0

MUSCL

MOOD- \mathbb{P}_3 U2

MOOD- \mathbb{P}_5 U2

II Cyclic remap — 128 cells/640 remaps — Unlim \mathbb{P}_5 , MUSCL, \mathbb{P}_5 MOOD with DMP, GLB, U2

UNLIM. \mathbb{P}_5

MOOD- \mathbb{P}_5 GLB

MOOD- \mathbb{P}_5 DMP

MOOD- \mathbb{P}_5 U2

III Cyclic remap — 64, 128, 256 cells/320, 640, 1280 remaps — \mathbb{P}_5 MOOD with U2

MOOD \mathbb{P}_3 64 cells

MOOD- \mathbb{P}_5 128 cells

MOOD- \mathbb{P}_5 64 cells

MOOD- \mathbb{P}_5 256 cells

High-order remapping

a posteriori MOOD. Euler equation.

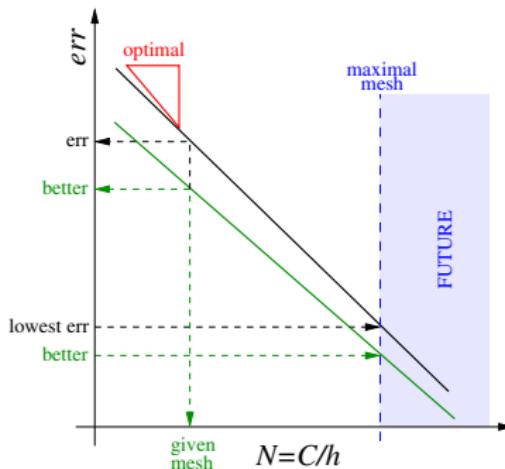
ALE = CC-Lagrangian (PL+lim) + Rezone + Remap,

Euler = CC-Lagrangian + Remap

Building a high-order remapping procedure is tempting. Classical Lagrangian schemes are nominally of 2nd order (space/time).

What's the point of high-order (MOOD) remapping ?

- Lagrangian scheme of order greater than 2 are on the way (Vilar, Kolev, Boscheri talks)
- Even if the order of convergence is nominally 2 what matters is the effective error at maximal available resolution
- Although the order of convergence is nominally 2 it is at most ~ 1 (3D, disc.). Discussing the order of convergence alone is incongruous.
- Black-box remapper of high-order may be useful to switch from code to code
- MOOD : one polynomial reconstruction per cell/variable. \neq from (W)ENO limitation Cheng, Shu in Applied Numerical Mathematics 58, 2008



High-order remapping

a posteriori MOOD. Euler equation.

Remapping of interleaved variables

Primitive variables are $(\rho, \mathbf{U} = (u, v), \varepsilon)$ and conservative ones are $(m, \mathbf{Q} = m\mathbf{U}, E)$ with

$$E = m(\varepsilon + \frac{1}{2}\|\mathbf{U}\|^2), \quad \text{and} \quad p = P(\rho, \varepsilon), \quad \text{and} \quad \rho > 0, \quad \varepsilon > 0$$

Sketch of remapping of conservative variables from \mathcal{M} onto $\widetilde{\mathcal{M}}$

$$\begin{array}{ccccccc} \text{Primitive} & \longrightarrow & \text{Conservative} & \text{REMAP} & \text{Conservative} & \longrightarrow & \text{Primitive} \\ (\rho_c, \mathbf{U}_c, \varepsilon_c) & \longrightarrow & (m_c, \mathbf{Q}_c, E_c) & \longrightarrow & (\tilde{m}_c, \tilde{\mathbf{Q}}_c, \tilde{E}_c) & \longrightarrow & (\tilde{\rho}_c, \tilde{\mathbf{U}}_c, \tilde{\varepsilon}_c) \end{array}$$

Conservation (global/local) and Admissibility

- $\mathbb{M} = \sum_c m_c = \sum_c \tilde{m}_c = \widetilde{\mathbb{M}}, \quad \mathbb{Q} = \sum_c m_c \mathbf{U}_c = \sum_c \tilde{\mathbf{Q}}_c = \widetilde{\mathbb{Q}}, \quad \mathbb{E} = \sum_c E_c = \sum_c \tilde{E}_c = \widetilde{\mathbb{E}}$
 - $\tilde{\rho}_c = \tilde{m}_c / \tilde{V}_c > 0, \quad \|\tilde{\mathbf{U}}_c\| = \|\tilde{\mathbf{Q}}_c / \tilde{m}_c\| < c^{\text{light}}, \quad \tilde{\varepsilon}_c = \tilde{E}_c / \tilde{m}_c - \frac{1}{2} \tilde{\mathbf{Q}}_c^2 / \tilde{m}_c + \Delta \mathbf{U}_c > 0$
- | | | |
|------|---------------|---------------------|
| easy | never checked | difficult to handle |
|------|---------------|---------------------|

High-order remapping

a posteriori MOOD. Euler equation.

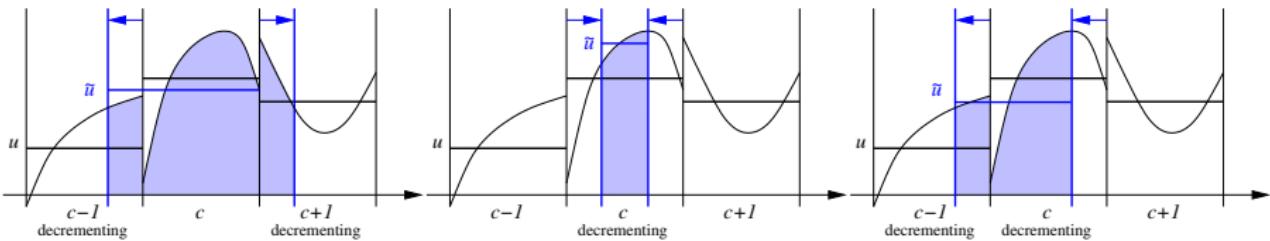
Classical nominally 2nd order remapper (PL reconstruction with limitation of variables)

Remap mass, momentum and energy (total or kinetic/internal). Expect density ρ_c in numerical bounds, velocity components U_c in bounds, internal energy ε_c positive. What if $\varepsilon_c < 0$?

High-order remapper with *a posteriori* MOOD — Mimick MOOD finite volume scheme

Remap with polynomial reconstruction with degree $d_c \rightarrow$ remapped candidate solution.
Detection criteria \mathcal{D}

- Physical Admissible Detection (PAD) : $0 \leq \tilde{\rho}_c$, and, $0 \leq \tilde{\varepsilon}_c$ (or pressure)
- Numer. Adm. Detect. (NAD) on ρ
 - 1 DMP violation : $\min_{j \in \nu_c}(\tilde{\rho}_j) \leq \tilde{\rho}_c \leq \max_{j \in \nu_c}(\tilde{\rho}_j)$? \rightarrow Possible problem
 - 2 Numer. smoothness and non-oscillation detection so-called U2 $\rightarrow d_c$ decrementing



High-order remapping

a posteriori MOOD. Euler equation. 1D ALE code

1D cell-centered ALE code

Cell-centered Lagrangian scheme (2nd order space/time).

- Goal : test the high-order MOOD remapping within the ALE framework.
- Methodology : Lagrange+Remap regime to emphasize the remapping behaviors as a function of mesh size (under- ultra-resolved), detection criteria (DMP, DMP+U2), cascade of schemes.
- Remappers :

MUSCL : classical PL reconstruction + limitation

\mathbb{P}_0 : donor cell remapper

MOOD \mathbb{P}_1 : cascade $\mathbb{P}_1 \rightarrow \mathbb{P}_0$

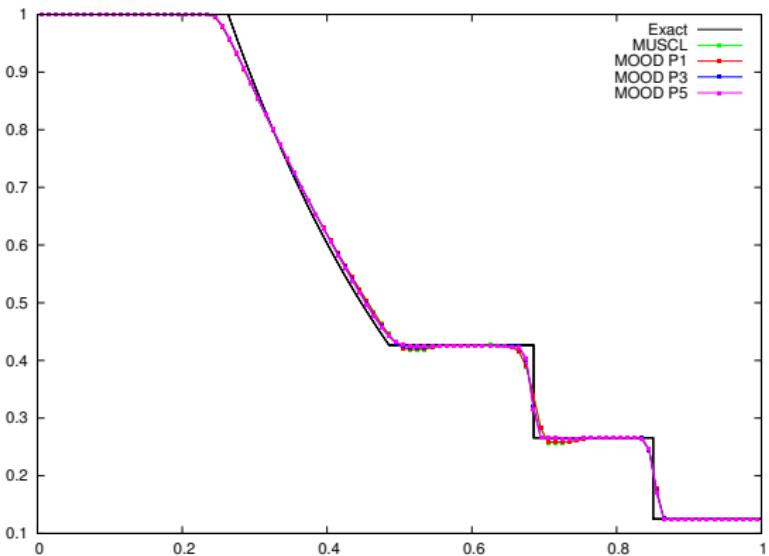
MOOD \mathbb{P}_k : cascade $\mathbb{P}_k \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$ or $\mathbb{P}_k \rightarrow \dots \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_1 \rightarrow \mathbb{P}_0$

Test cases

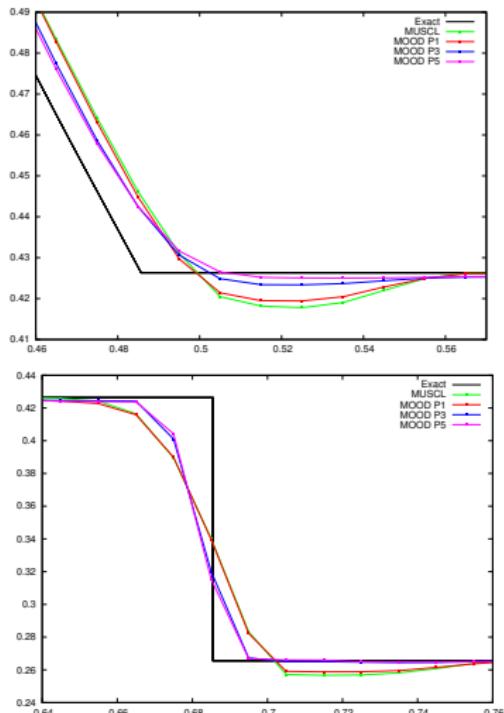
Sod tube, 123 problem (double rarefaction), Colella-Woodward blastwave

1D Lag+Remap with high-order MOOD remapping

Sod tube 100 cells — MUSCL, MOOD $\mathbb{P}_1, \mathbb{P}_3, \mathbb{P}_5$

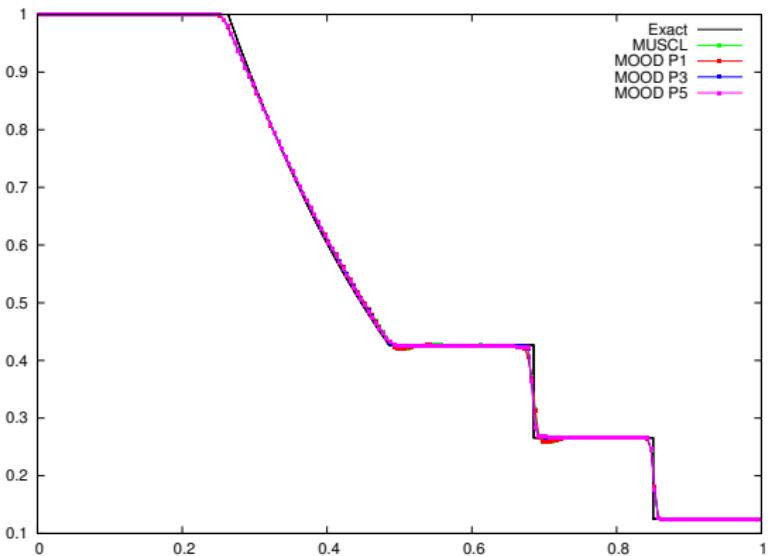


MUSCL : \mathbb{P}_1 with limiter,
 MOOD \mathbb{P}_1 : $\mathbb{P}_1 \rightarrow \mathbb{P}_0$,
 MOOD \mathbb{P}_{\max} : $\mathbb{P}_{\max} \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$,
 Detection criteria : DMP+U2 on ρ

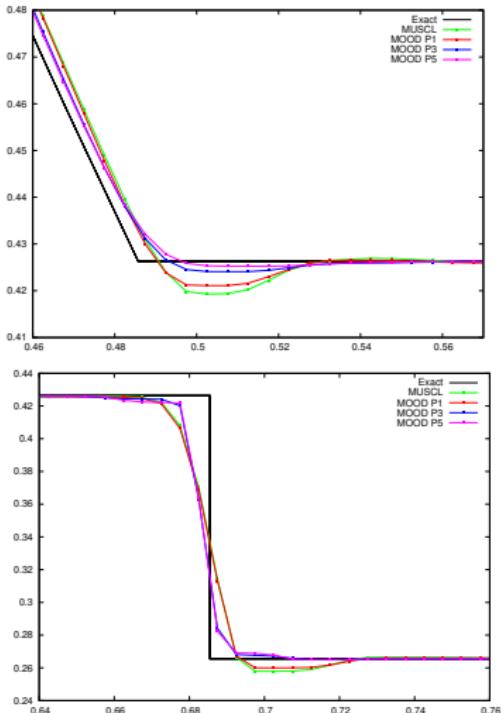


1D Lag+Remap with high-order MOOD remapping

Sod tube 200 cells — MUSCL, MOOD $\mathbb{P}_1, \mathbb{P}_3, \mathbb{P}_5$



MUSCL : \mathbb{P}_1 with limiter,
 MOOD \mathbb{P}_1 : $\mathbb{P}_1 \rightarrow \mathbb{P}_0$,
 MOOD \mathbb{P}_{\max} : $\mathbb{P}_{\max} \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$,
 Detection criteria : DMP+U2 on ρ



1D Lag+Remap with high-order MOOD remapping

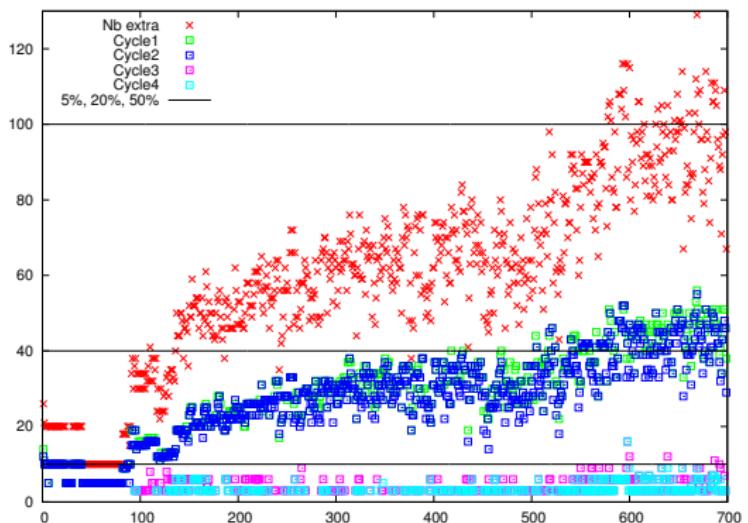
Sod tube 200 cells — MOOD \mathbb{P}_3 — Cell polynomial degrees

$$\mathbb{P}_3 \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$$

$$\mathbb{P}_3 \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_1 \rightarrow \mathbb{P}_0$$

1D Lag+Remap with high-order MOOD remapping

Sod tube 200 cells — Extra remapping — MOOD \mathbb{P}_3



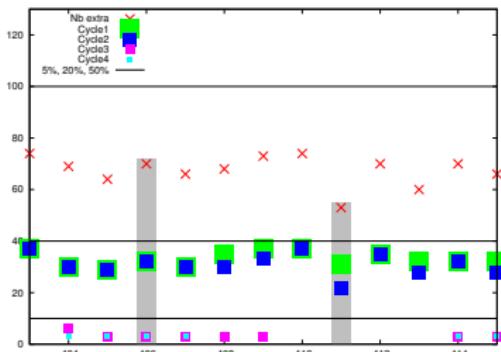
x-axis : time iterate, y-axis : nb of remapped cells

Cycle0 : \mathbb{P}_3 for 200 cells, Cycle1 : \mathbb{P}_2 for N_1 cells,

Cycle2 : \mathbb{P}_2 or \mathbb{P}_0 for N_2 cells, etc.

Extra cost : Nb extra remaps = $N_1 + N_2 + \dots$

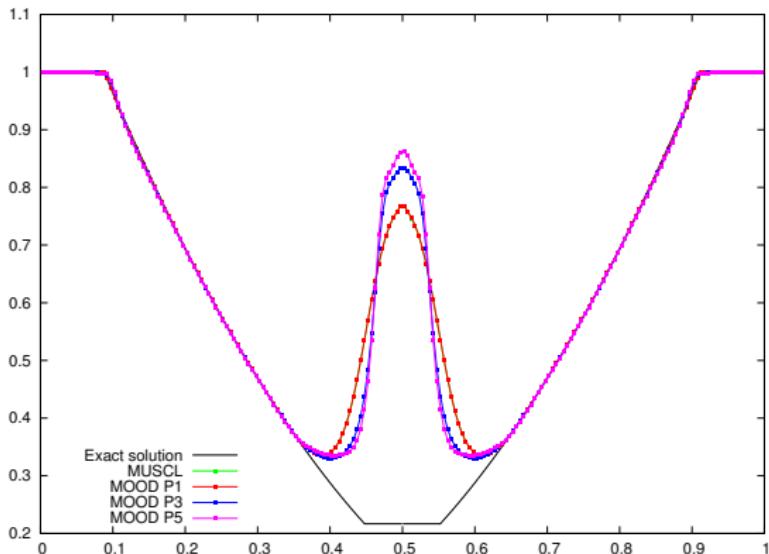
Zoom and two examples



Iter	Tot	#1	#2	#3	#4
406	70	32	32	3	3
411	53	31	22	—	—

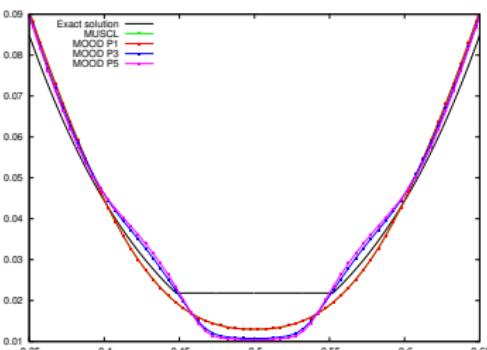
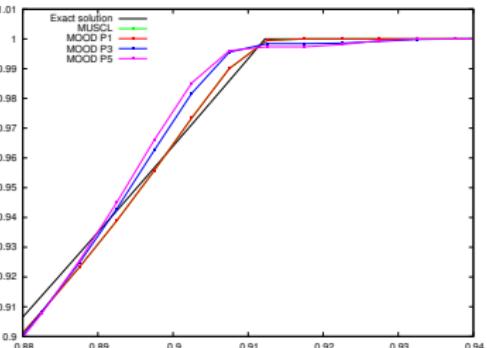
1D Lag+Remap with high-order MOOD remapping

Double rarefaction 200 cells — MUSCL, MOOD $\mathbb{P}_1, \mathbb{P}_3, \mathbb{P}_5$



MUSCL : \mathbb{P}_1 with limiter,
 MOOD \mathbb{P}_1 : $\mathbb{P}_1 \rightarrow \mathbb{P}_0$,
 MOOD \mathbb{P}_{\max} : $\mathbb{P}_{\max} \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$,
 Detection criteria : DMP+U2 on ρ

Zoom on ε (head) and ρ (central)



1D Lag+Remap with high-order MOOD remapping

Double rarefaction 200 cells — MOOD \mathbb{P}_5 — Cell polynomial degrees

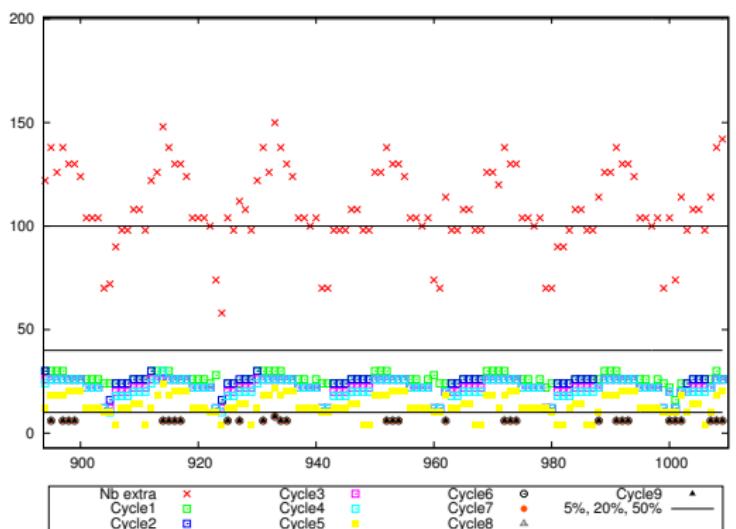
$$\mathbb{P}_5 \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$$

$$\mathbb{P}_5 \rightarrow \mathbb{P}_4 \rightarrow \mathbb{P}_3 \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_1 \rightarrow \mathbb{P}_0$$

Note that decrementing occurs “a lot” on plateaus !

1D Lag+Remap with high-order MOOD remapping

Double rarefaction 200 cells — Extra remapping — MOOD $\mathbb{P}_{5,4,3,2,1,0}$

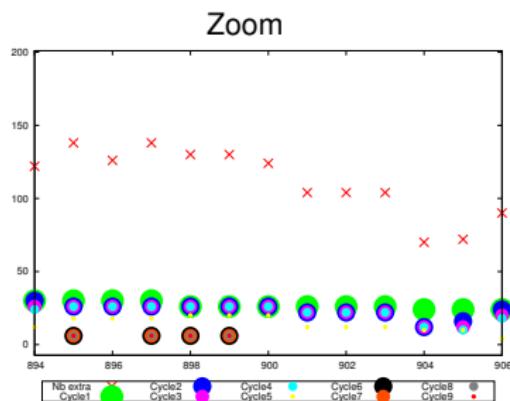


x-axis : time iterate, y-axis : nb of remapped cells

Cycle0 : \mathbb{P}_5 for 200 cells, Cycle1 : \mathbb{P}_4 for N_1 cells,

Cycle2 : $\mathbb{P}_4/\mathbb{P}_3$ or \mathbb{P}_0 for N_2 cells, etc.

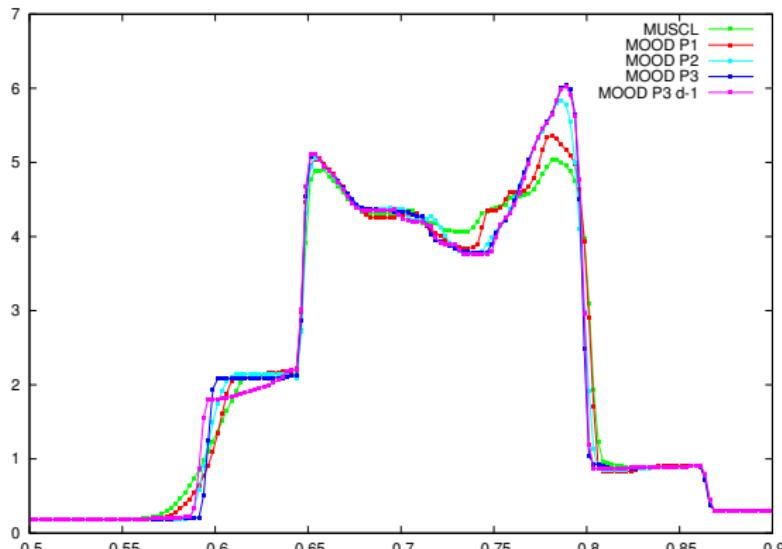
Extra cost : Nb extra remaps = $N_1 + N_2 + \dots$



More cycles do not improve the quality of the results and waste CPU time.

1D Lag+Remap with high-order MOOD remapping

Blastwave 400 cells — MUSCL, MOOD $\mathbb{P}_3, \mathbb{P}_2, \mathbb{P}_1$



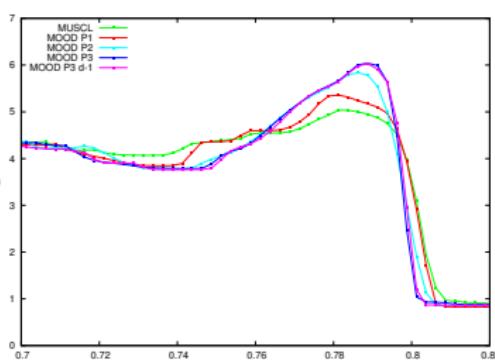
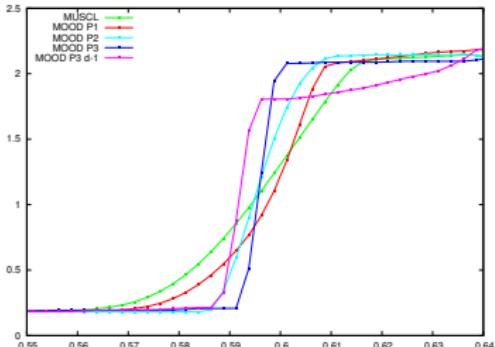
MUSCL : \mathbb{P}_1 with limiter,

MOOD \mathbb{P}_1 : $\mathbb{P}_1 \rightarrow \mathbb{P}_0$, MOOD \mathbb{P}_{\max} : $\mathbb{P}_{\max} \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$,

MOOD \mathbb{P}_{\max} d-1 : $\mathbb{P}_3 \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_1 \rightarrow \mathbb{P}_0$

Improvement while beneath still 2nd order Lag. scheme.

Zoom on left contact and peak



1D Lag+Remap with high-order MOOD remapping

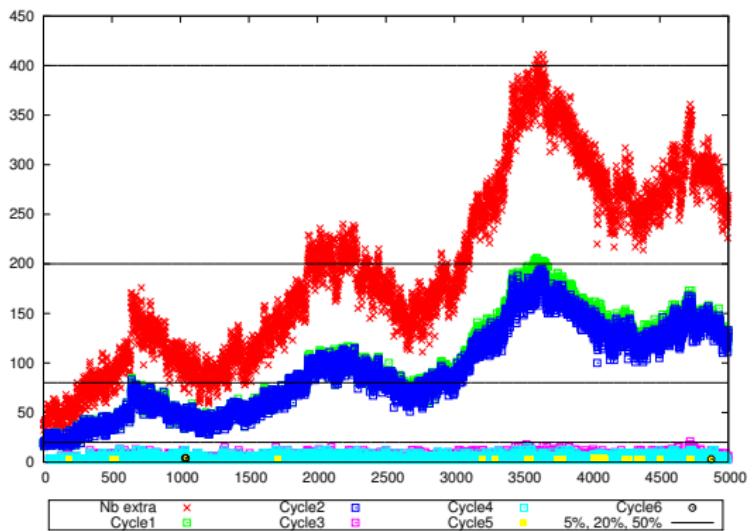
Blastwave 400 cells — MOOD \mathbb{P}_3 — Cell polynomial degrees

$$\mathbb{P}_3 \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_0$$

$$\mathbb{P}_3 \rightarrow \mathbb{P}_2 \rightarrow \mathbb{P}_1 \rightarrow \mathbb{P}_0$$

1D Lag+Remap with high-order MOOD remapping

Blastwave 400 cells — MOOD \mathbb{P}_3 — Cell polynomial degrees

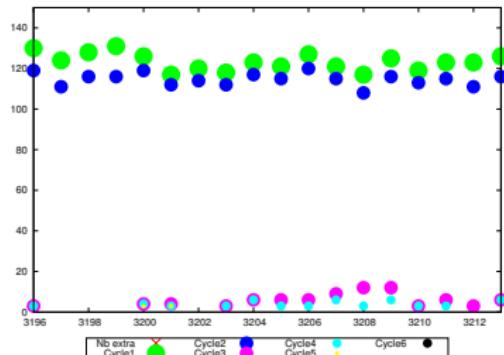


x-axis : time iterate, y-axis : nb of remapped cells

Cycle0 : \mathbb{P}_5 for 200 cells, Cycle1 : \mathbb{P}_2 for N_1 cells,
Cycle2 : $\mathbb{P}_2/\mathbb{P}_0$ for N_2 cells, etc.

Extra cost : Nb extra remaps = $N_1 + N_2 + \dots$

Zoom



Iter	Tot	#1	#2	#3	#4	#5
3200	255	126	119	4	4	3

Cycles are pairing up. $\sim 20\%$ (cycle 1 and cycle 2), $\sim 2\%$ (cycle 3+)

Conclusion and perspectives

High-order MOOD like remapping

- Construct one conservative polynomial per degree, per cell. No choice of stencil, no *a priori* limitation.
- Unlimited remap. Detect (DMP+U2) problematic cells for which degree decrementing occurs. Iterative remap of problematic cells until validity or \mathbb{P}_0 .
- Detection criteria, cascade of scheme and final parachute scheme are user-choices

Numerical results

- Static remapping of passive scalar shows improvement when using high-order polynomials. Though weird behaviors may occur.
- Dynamic remapping of system of interleaved variables (1D Euler equations in ALE regime). Cannot expect extreme improvement though nice behaviors are already observed.

Next

- More testing in 2D ALE.
- MOOD HO finite volume with S.Clain, S.Diot, M.Dumbser for different systems - astrophysics, MHD, etc. See talk of S.Diot : "MOOD multimaterials".

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www.agence-nationale-recherche.fr / The young investigator program JCJC has funded the project 'ALE INC(ubator) 3D'.
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- French embassy in Prague Czech Republic

Vacation conference in Spain next July ?

Minisymposium : “[New trends in Numerical Methods for Multi-Material Compressible Fluid Flows](#)”
Barcelona, Spain, July 2014 during IACM and ECCOMAS conferences
(www.wccm-eccm-ecfd2014.org). We are expecting you !

Thank you for your attention.
Merci de votre attention.